WHAT IS CLAIMED IS:

1. A GENE-TAG reporter, suitable for joining to a probe either alone or in combination with another GENE-TAG reporter, comprising a labeled, double-stranded polynucleotide sequence having one or more first linkers, said first linker comprising a single-stranded nucleotide sequence hybridizable to a complementary single-stranded nucleotide sequence, wherein said first linkers is not hybridizable to a target sequence of said probe.

2. The GENE-TAG of Claim 1, wherein said GENE-TAG further comprises one or more second linkers opposed to said first linker, said second linker comprising a single-stranded nucleotide sequence hybridizable to a complementary nucleotide sequence, wherein said second linker is not hybridizable to a target sequence of said probe.

3. The GENE-TAG of Claim 2, wherein said first and second linkers are complementary.

4. A reporter array, suitable for joining to a probe, comprising two or more of the GENE-TAGs of Claim 3, linked together end-to-end by hybridization of the second linker of a first GENE-TAG to the first linker of a second GENE-TAG, and optionally, additional GENE-TAGs linked to the remainder of the array by hybridization of the first linker of each subsequent GENE-TAG to the second linker of the preceding GENE-TAG in the array, to form a chained or branched configuration having one or more terminal ends, said terminal end comprising a second linker of a terminal GENE-TAG.

5. The reporter array of Claim 4, further comprising one or more terminators, wherein said terminator comprises a single-stranded nucleotide sequence complementary to the second linker of one or more terminal GENE-TAGs, whereby said terminator forms said terminal end.

6. The GENE-TAG of Claim 2, wherein the first and second reporter linkers are not complementary.

7. A reporter array, suitable for joining to a probe, said reporter array comprising two or more of first GENE-TAGs of Claim 6, linked indirectly by one or more second GENE-TAGs of Claim 6 by end-to-end hybridization of the second linker of a first GENE-TAG to the first linker of a second GENE-TAG, and hybridization of the second linker of a second GENE-TAG to the first linker of said first GENE-TAG, and optionally, additional non-complementary GENE-TAGs linked to the remainder of the array by hybridization of the first linker of each subsequent GENE-TAG to the complementary second linker of the preceding GENE-TAG in the array, to form a chained or branched configuration.

8. A probe, suitable for hybridizing to a target nucleotide sequence, said probe comprising a first terminal linker, a second terminal linker, and a central sequence complementary to said target nucleotide sequence, wherein said first and second terminal linkers comprise single-stranded nucleotide sequences hybridizable to a complementary nucleotide sequence, but not hybridizable to the target nucleotide sequence of said probe.

9. A composite probe, suitable for hybridizing to a target nucleotide sequence, comprising at least one probe, said probe comprising a polynucleotide sequence complementary to said target nucleotide sequence, said composite probe further comprising a polynucleotide ring unit, wherein said polynucleotide ring unit is joined to said probe to form an incipient closed loop.

10. The composite probe of Claim 9, comprising a first and second probe, wherein said first probe comprises a sequence complementary to a first region of said target nucleotide sequence, and wherein said second probe comprises a sequence complementary to a second region of said target sequence, wherein said ring unit is joined to said first probe and to said second probe, thereby forming an incipient closed loop.

11. A Multi-LINKER multi-linking unit, which allows two or more reporters to be bound to a probe, comprising a first polynucleotide comprising a first terminal linker, a second terminal linker, and at least one internal linker, wherein said first terminal linker, and at least two of said internal and second terminal linkers are hybridizable to complementary nucleotide sequences, and wherein said first and second terminal linkers and said internal linker are not hybridizable to a target sequence of said probe.

12. The Multi-LINKER of Claim 11, further comprising one or more additional polynucleotides, said additional polynucleotide comprising a first terminal linker, at least one internal linker, and a second terminal linker, wherein the first polynucleotide is joined to the additional polynucleotides by hybridization of the additional polynucleotide to the internal or second terminal linker of the first polynucleotide, and wherein said first and second terminal linkers and said internal linker are not hybridizable to a target sequence of said probe.

13. A GAP-LOCK method for detecting a target nucleotide sequence, comprising the steps of:

a) rendering the target nucleotide sequence substantially single-stranded to give a single-stranded target nucleotide sequence;

b) hybridizing the target sequence with a first probe and with a second probe, wherein said first and second probes hybridize at tandem locations on the target nucleotide sequence, wherein each of said first and second probes comprises a proximal ligation end and wherein one or both of said first or second probes further comprises a distal linker, said distal linker comprising a single-stranded nucleotide sequence that does not hybridize to the target nucleotide sequence; wherein said distal linker is joined to one or more reporters, either prior to or subsequent to the hybridization of the first and second probes to the target sequence;

c) ligating the hybridized first and second probes at their respective proximal ligation ends to form a composite probe structure known as a GAP-LOCK probe:

d) joining said reporter or reporters to said distal linker, if not previously joined;

e) denaturing to remove any unligated first and second probe;

f) determining whether the target nucleotide sequence is present by detecting the presence or absence of said reporter or reporters.

14. The method of claim 13, wherein one of said first or second probes comprises a distal linker.

15. The method of claim 13, wherein said first probe comprises a first distal linker, and wherein said second probe comprises a second distal linker.

16. The method of claim 15, wherein the first and second distal probe linkers have a common sequence and orientation.

17. A RING-LOCK method for providing circular enclosure of a target strand by a composite probe, comprising:

a) providing a target strand comprising a target sequence;

b) providing the first and second probe of Claim 15,

c) providing a RING-TAIL Unit comprising at least three single-stranded polynucleotides, wherein at least one single-stranded polynucleotide is joined or suitable for joining to the first distal linker, and wherein at least one single-stranded polynucleotide is joined or suitable for joining to said second distal linker; and wherein at least one single-stranded polynucleotide is joined or suitable for joining to one or more reporters;

d) rendering or treating said probes and said RING-TAIL Unit to effect cross linking or to increase binding;

e) hybridizing the first and second probe to the target, thereby forming a hybridized complex;

f) ligating said first and second probes, thereby forming a closed loop or an incipient closed loop around the target strand;

g) hybridizing at least one single-stranded polynucleotide to said first distal probe linker, if not previously joined; hybridizing at least one single-stranded polynucleotide to said second distal probe linker, if not previously joined;

h) hybridizing a reporter or reporters to at least one single-stranded polynucleotide, if not previously attached, or if necessary;

i) denaturing or washing the hybridized complex to remove unligated probe and reporters;

j) detecting the presence of reporters to indicate the target sequence.

18. A method of simultaneously detecting a target sequence on both a sense and an antisense strand of DNA, known as a DOUBLE RING-LOCK method, comprising:

a) providing a double-stranded DNA comprising a sense target strand and an antisense target strand, wherein said sense target strand comprises a sense target sequence, and wherein said antisense target strand comprises an antisense target sequence;

b) providing a first sense probe and a second sense probe of Claim 15;

c) providing a first antisense probe and a second antisense probe of Claim 15;

d) providing a first RING-TAIL Unit comprising at least three first single-stranded nucleotides, wherein at least one said first single-stranded nucleotide is joined or suitable for joining to said first distal linker of said sense first probe, and wherein at least one said first single-stranded nucleotide is joined or suitable for joining to said first distal linker of said second sense probe, and wherein at least one first single stranded nucleotide is joined or suitable for joining to one or more first reporters;

e) providing a second RING-TAIL Unit, comprising at least three second single-stranded polynucleotides, wherein at least one said second single-stranded polynucleotide is joined or suitable for joining to said first distal linkerof said antisense first probe, and wherein at least one said second single-stranded polynucleotide is joined or suitable for joining to said first distal probe linker of said second antisense probe, and wherein at least one second single stranded polynucleotide is joined or suitable for joining to one or more second

reporters, wherein said second reporter produces a signal distinct from a signal produced by said first reporter;

(f) treating the probes and RING-LOCK Units, at this step or another step, to effect cross linking or to increase binding;

(g) hybridizing said first and second sense probes to the sense strand, thereby forming a sense hybridized complex; and hybridizing said first and second antisense probes to the antisense strand, thereby forming an antisense hybridized complex;

(h) ligating said first and second sense probes, thereby forming a closed loop or an incipient closed loop around the sense target strand; and ligating said first and second antisense probes, thereby forming a closed loop or an incipient closed loop around the antisense target strand;

(i) joining at least one first single-stranded polynucleotide to said first distal linker of said first sense probe, if not previously joined; joining at least one first single-stranded polynucleotide to said second distal linker of said second sense probe, if not previously joined; joining at least one second single stranded polynucleotide to said first distal linker of said first antisense probe, if not previously joined; joining at least one second polynucleotide to said second distal linker of said second antisense probe, if not previously joined;

(j) joining one or more first reporters to at least one said first single-stranded polynucleotide, if not so previously joined; joining one or more second reporters to at least one said second single-stranded polynucleotide, wherein said second reporter produces a signal distinct from said first reporter;

(k) determining whether the sense target sequence is present by detecting the presence or absence of said first reporter or reporters; or determining whether the antisense target sequence is present by detecting the presence or absence of said second reporter or reporters; or both.

19. The method of Claim 14, for use under liquid or near-liquid hybridization conditions, wherein said first probe comprises a distal end that is joined to a capture moiety, and said

second probe has a second distal linker, further comprising denaturing to remove the target sequence, and capturing the GAP-LOCK probe to detect the reporter.

20. The method of claim 15, wherein said first probe further comprises a capture moiety joined to said first distal linker, further comprising denaturing to remove the target sequence, and capturing the GAP-LOCK probe to detect the reporter.

21. A GAP-LOCK method for detecting a target nucleotide sequence, comprising:

a) rendering the nucleotide sequence substantially single-stranded to give a single-stranded nucleotide sequence;

b) hybridizing the target sequence with a first probe and a second, wherein said first and second probes hybridize at tandem locations on the target, wherein each of said first and second probes comprises a proximal ligation end, and a distal end pre-joined to one or more reporters;

c) ligating the hybridized first and second probes at their respective proximal ligation ends to form a GAP-LOCK probe;

d) denaturing or washing to remove any unligated first and second probe;

e) determining whether the target nucleotide sequence is present by detecting the presence or absence of said reporter or reporters.

22. The method of Claim 21, wherein said distal end is pre-joined directly to a first reporter comprising a labeled, double-stranded polynucleotide generated by PCR.

23. The method of Claim 22, wherein said first reporter further comprises one or more distal reporter linkers, said distal reporter linker comprising a single-stranded nucleotide sequence hybridizable to a complementary nucleotide sequence, said distal reporter linker not hybridizable to the target nucleotide sequence.

24. The method of claim 23, further comprising a labeled, double-stranded DNA sequence, known as a GENE-TAG, comprising one or more first reporter linkers, said first

reporter linker comprising a single-stranded nucleic acid sequence hybridized to the distal reporter linker of said first reporter.

25. The method of claim 23, further comprising a reporter array, said reporter array comprising a first labeled, double-stranded polynucleotide sequence, known as a GENE-TAG, linked together end-to-end by hybridization to one or more GENE-TAGS, wherein said first GENE-TAG comprises one or more first reporter linkers, said reporter linker comprising a single-stranded nucleotide sequence hybridizable to the distal reporter linker of said first reporter, and one or more second reporter linkers hybridized to one or more first reporter linkers of a second GENE-TAG, and wherein said second GENE-TAG further comprises one or more second reporter linkers, and optionally, additional GENE-TAGs linked to the remainder of the array by hybridization of the first reporter linker of each subsequent GENE-TAG to the second reporter linker of the preceding GENE-TAG in the array, to form a chained or branch configuration having one or more terminal ends, said terminal end comprising the second reporter linker of a terminal GENE-TAG.

26. The method of Claim 25, further comprising one or more terminators, wherein said terminator comprises a single-stranded polynucleotide sequence complementary to the second reporter linker of one or more terminal GENE-TAGs, whereby said terminator forms said terminal end.

27. The method of Claim 21, for use under liquid or near-liquid hybridization conditions, wherein said first probe comprises a distal end that is joined to a capture moiety, and said second probe has a distal end attached to one or more reporters, further comprising denaturing to remove the target sequence, and capturing the GAP-LOCK probe to detect the reporter.

28. A WRAP-PROBE method for detecting a target nucleotide sequence, comprising:

a) rendering the target nucleotide sequence substantially single-stranded to give a single-stranded target nucleotide sequence;

b) hybridizing the single-stranded target nucleotide sequence with a nucleic acid probe, thereby forming a hybridized WRAP-PROBE complex of a single-

stranded target nucleotide sequence and a nucleic acid probe, said WRAP-PROBE comprising a central sequence complementary to the single-stranded target nucleotide sequences, and further comprising a probe linker at one or both terminal ends, said probe linker comprising a single-stranded nucleotide sequence that does not hybridize to the target sequence; wherein said probe linker sequence is joined to one or more reporters, either prior to or subsequent to the hybridization of the probe to the target sequence;

c) washing to remove any unbound probe;

d) joining said reporter to said probe linker, if not previously joined;

e) detecting the presence or said reporter or reporters to indicate the target sequence.

29. The method of Claim 28, wherein the probe comprises a first terminal probe linker.

30. The method of Claim 28, wherein the probe comprises a first terminal probe linker and a second terminal probe linker.

31. The method of Claim 30, wherein the reporter is a labeled, double-stranded polynucleotide sequence, known as a GENE-TAG, having one or more said first reporter linkers, said first reporter linker comprising a single-stranded nucleotide sequence hybridized to the first terminal probe linker.

32. The method of Claim 30, wherein one or more reporters comprise a reporter array, said array comprising a first labeled, double-stranded polynucleotide sequence, known as a GENE-TAG, linked together end-to-end by hybridization to one or more GENE-TAGS, wherein said first GENE-TAG comprises one or more first reporter linkers, said first reporter linker comprising a single-stranded nucleotide sequence hybridizable to said first terminal probe linker, and one or more second reporter linkers hybridized to one or more first reporter linkers of a second GENE-TAG, and wherein said second GENE-TAG further comprises one or more second reporter linkers, and optionally, additional GENE-TAGs linked to the remainder of the array by hybridization of the first reporter linker of each subsequent GENE-

TAG to the second reporter linker of the preceding GENE-TAG in the array, to form a chained or branch configuration having one or more ends, wherein said terminal end comprises the second reporter linker of a terminal GENE-TAG.

33. The method of Claim 32, further comprising one or more terminators, said terminator comprising a single-stranded polynucleotide sequence complementary to said second reporter linker of one or more terminal GENE-TAGs, such that said terminator forms said terminal end.

34. The method of Claim 28, wherein the reporter is joined directly to the first terminal probe linker.

35. The method of Claim 28, wherein the reporter is joined indirectly to the first terminal probe linker, further comprising a multi-linking unit interposed between said reporter and terminal probe linker, said unit known as a Multi-LINKER, comprising a first polynucleotide comprising a first terminal unit linker, a second terminal unit linker, and at least one internal linker, wherein said first terminal unit linker is hybridized to said first terminal probe linker, and wherein at least two of said internal and second terminal unit linkers are hybridized to one or more reporters, and wherein said first and second terminal unit linkers and said internal linker are not hybridizable to a target sequence of said probe.

36. The method Claim 35, further comprising ~~one or more~~ additional polynucleotides, said additional polynucleotide comprising a first terminal unit linker, a second terminal unit linker, and at least one internal linker, wherein the first polynucleotide is joined to the additional polynucleotide by hybridization of the additional polynucleotide to the internal or second terminal linker of the first polynucleotide, and wherein said first and second terminal linkers and said internal linker are not hybridizable to a target sequence.

37. The method of Claim 30, wherein the reporter is a short oligonucleotide having a label unit.

38. A WRAP-LOCK method for providing circular enclosure of the target polynucleotide strand with a WRAP-PROBE, comprising:

a) providing the WRAP-PROBE of Claim 30;

b) providing a RING-LOCK Unit comprising at least two single-stranded polynucleotides, wherein at least one single-stranded polynucleotide is joined or suitable for joining to said first terminal probe linker, and wherein at least one single-stranded polynucleotide is joined or suitable for joining to one or more reporters;

c) treating the probe and RING-TAIL unit, at this step or another step, to effect cross linking or to increase binding;

c) hybridizing the WRAP-PROBE to the target strand, thereby forming a hybridized complex;

d) joining at least one single-stranded polynucleotide to said first terminal probe linker, if not previously joined,

e) providing a looping polynucleotide comprising a first region complementary to said second terminal probe linker, and a second region complementary to said RING-TAIL Unit, wherein said looping polynucleotide hybridizes to the second terminal probe linker and the RING-TAIL Unit, thereby forming a closed loop about the target strand;

f) joining a reporter or reporters to at least one ring-tail linker, if not previously attached; and

g) detecting the presence of reporter to indicate the target sequence.

39. A DOUBLE WRAP-LOCK method of simultaneously detecting a target sequence on both a sense and anti-sense strand of DNA, comprising:

a) providing a double-stranded DNA comprising an antisense strand and a sense strand, wherein both said antisense strand and said sense strand comprise a target sequence;

b) providing a sense WRAP-PROBE of Claim 30, said sense WRAP-PROBE probe having a central sequence complementary to the sense strand target sequence;

c) providing an antisense WRAP-PROBE probe of Claim 30, said antisense WRAP-LOCK probe having a central sequence complementary to the antisense strand target sequence;

d) providing a first RING-TAIL Unit comprising at least two first single-stranded polynucleotides, wherein at least one first single-stranded polynucleotide is joined or suitable for joining to said first terminal probe linker of said sense WRAP-PROBE, and wherein at least one first single-stranded polynucleotide is joined or suitable for joining to one or more first reporters;

e) providing a second RING-LOCK Unit comprising at least two second single-stranded polynucleotides, wherein at least one second single-stranded polynucleotide is joined or suitable for joining to said first terminal probe linker of said antisense WRAP-PROBE, and wherein at least one second single-stranded polynucleotide is joined or suitable for joining to one or more second reporters, wherein said second reporter produces a signal distinct from said first reporter;

(f) treating the WRAP-PROBEs and the RING-LOCK Units, at this step or another step, to effect cross linking or to increase binding;

(g) hybridizing said sense WRAP-PROBE to the sense strand, thereby forming a sense hybridized complex; and hybridizing said antisense WRAP-PROBE to the antisense strand, thereby forming an antisense hybridized complex;

(h) joining at least one first single-stranded polynucleotide to said first terminal probe linker of said sense WRAP-PROBE, if not so previously joined; and joining at least one second single-stranded polynucleotide to said first terminal probe linker of said antisense WRAP-PROBE, if not so previously joined;

(i) providing a first looping polynucleotide comprising a first region complementary to said second terminal probe linker of said sense WRAP-PROBE, and a second region complementary to said first RING-TAIL Unit, wherein said looping polynucleotide hybridizes and thereby forms a closed loop about the target sense strand; and providing a second looping polynucleotide comprising a first region complementary to said second terminal probe linker of said antisense WRAP-PROBE, and a second region complementary to said second RING-TAIL Unit, wherein said looping

polynucleotide hybridizes and thereby forms a closed loop about the target antisense strand;

(j) joining one or more first reporters to at least one said first single-stranded polynucleotide, if not so previously joined; joining one or more second reporters to at least one said second single-stranded polynucleotide, if not previously joined, wherein said second reporter produces a signal distinct from said first reporter;

(k) determining whether the sense target sequence is present by detecting the presence or absence of said first reporter or reporters; or determining whether the antisense target sequence is present by detecting the presence or absence of said second reporter or reporters, or both.

40. A GENE-TAG method for exponential signal amplification for the detection of a target nucleotide sequence, comprising:

a) providing a single-stranded target nucleic acid sequence;

b) providing a probe comprising a sequence hybridizable to said target nucleic acid sequence, and a terminal linker sequence on one or both ends of the probe, wherein said linker sequence is a single-stranded polynucleotide hybridizable to a complementary sequence;

c) providing one or more GENE-TAGs, said GENE-TAG comprising a labeled, ~~double-stranded~~ polynucleotide reporter having one or more first reporter linkers and one or more second reporter linkers ~~opposed to said first reporter~~ linker, said reporter linkers comprising single-stranded polynucleotide sequences not hybridizable to the target sequence, wherein at least one said GENE-TAG has a first reporter linker complementary to said probe terminal linker, and wherein one or more said reporter linkers link together end-to-end by hybridization of the first reporter linker of each subsequent GENE-TAG to the second reporter linker of each preceeding GENE-TAG in the array, to form a chained or branched configuration comprising one or more terminal end, wherein said terminal end comprises the second reporter linker of a terminal

GENE-TAG; wherein said GENE-TAG is joined to said probe in this or a subsequent step;

d) hybridizing said probe to said target nucleotide sequence;

e) joining said GENE-TAG or GENE-TAGs to said probe, if not so previously joined;

f) determining the presence of the target sequence by detecting the presence of the GENE-TAG or GENE-TAGs. .

41. The method of Claim 40, wherein the first and second reporter linkers of the GENE-TAGs are complementary, such that only GENE-TAGs of one type are required to form chained or branched reporter arrays.

42. The method of Claim 41, further comprising one or more terminators, said terminator comprising a single-stranded polynucleotide sequence complementary to said second reporter linker of said terminal GENE-TAG, such that said terminator forms said terminal end.

43. The method of Claim 42, wherein the length of said chained or branched reporter arrays, and thus probe amplification, is controlled by the ratio of GENE-TAGs to said terminators.

44. The method of Claim 41, further comprising a Terminator TAG, said Terminator TAG comprising a GENE-TAG having no second reporter linker, wherein said first reporter linker of said Terminator TAG hybridizes to the second reporter linker of a terminal GENE-TAG of the chain or branch.

45. The method of Claim 44, wherein the length of said chained or branched reporter arrays, and thus probe amplification, is controlled by the ratio of GENE-TAGs to Terminator TAG.

46. The method of Claim 40, wherein only one GENE-TAG is provided, said GENE-TAG having no second reporter linker.

47. The method of Claim 40, wherein said first and second linkers of said GENE-TAGs are not complementary, such that at least two types of GENE-TAGs are required to form chained or branched arrays, wherein GENE-TAGs of a first type comprise a first reporter linker complementary to the probe terminal linker, and a second reporter linker complementary to the first reporter linker of GENE-TAG of the second type, and wherein said GENE-TAG of the second type has a first reporter linker complementary to the second reporter linker of a GENE-TAG of the first type, such that only a GENE-TAG of the first type will bind to a GENE-TAG of the second type, and only a GENE-TAG of the second type will bind to a GENE-TAG of the first type; wherein said chained or branched arrays are formed by providing GENE-TAGs sequentially, alternating between the first and second type, and thereby forming alternating layers of GENE-TAGs of a first or second type upon the probe.

48. The method of Claim 40, wherein said GENE-TAGS are constructed by PCR amplification of arbitrary template DNA using one or more modified oligonucleotides as primers, wherein each modified oligonucleotide has one or more internal spacers, whereby the first and second terminal single-stranded linkers are preserved.

49. The method of Claim 40, wherein said GENE-TAGs are constructed by hybridization of two polynucleotides, said first polynucleotide having a second terminal end complementary to the first terminal end of a second polynucleotide.

50. The method of Claim 49, wherein said first polynucleotide has an internal sequence complementary to the internal sequence of a second polynucleotide, forming a GENE-TAG having side arms, said side arms comprising the second terminal end of the first polynucleotide, and the first terminal end of the second polynucleotide, said GENE-TAGs known as TINKER-TAGS.

51. The method of Claim 40, wherein the GENE-TAG is labeled directly.

52. The method of Claim 40, wherein the GENE-TAG is labeled indirectly.

53. The method of Claim 50, wherein said TINKER-TAGs are labeled indirectly by hybridization of said side arms to short oligonucleotides conjugated to one or more labeling agents.

54. The method of Claim 53, wherein said TINKER-TAGs are labeled indirectly by hybridization of said side arms to short oligonucleotides conjugated to gold particles, said gold particles coated in silver to form dense clusters.

55. A method of constructing probes detectable on the basis of a unique signal, comprising:

a) providing a probe hybridizable to a single-stranded nucleotide sequence, wherein said probe comprises a terminal linker at one or both ends, said terminal linker comprising a single-stranded polynucleotide capable of binding to a complementary sequence;

b) preparing one or more COLOR-TAGs, said COLOR-TAG comprising a double-stranded polynucleotide reporter having a first reporter linker and a second reporter linker opposed to said first reporter linker, wherein said COLOR-TAG is labeled with one or more labels or colors, or both, and wherein said first and second reporter linkers are specific to the labels or colors employed; wherein at least one COLOR-TAG terminal linker is hybridizable to the terminal linker of said probe;

c) hybridizing one or more of said COLOR-TAGs to the probe, at this step or a later step;

e) hybridizing said probe to said target sequence;

f) hybridizing said COLOR-TAG to the probe, if not so previously hybridized;

g) determining the presence of said target sequence by detecting the presence of said COLOR-TAG.

56. The method of Claim 55, wherein said Color-TAG is labeled with two or more different labels or colors.

57. The method of Claim 55, further comprising a multilinking unit suitable for joining said probe to one or more COLOR-TAGs, said multilinking unit comprising a proximal linker for joining said multilinking unit to said probe terminal linker, and one or more distal linkers known as COLOR-LINKERS, said COLOR-LINKERS complementary to one or more of said COLOR-TAG terminal linkers, wherein a specific mix of COLOR-TAGS is captured by said multilinking unit depending on the type and specific ratio of COLOR-LINKERS used to prepare the multilinking unit, wherein said multilinking unit is hybridized to said COLOR-TAGS, thereby forming a COLOR-TAG complex, either prior or subsequent to the hybridization of the multilinking unit to the probe, and wherein said multilinking unit is hybridized to said probe either prior to or subsequent to the hybridization of the probe to said target sequence.